

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 11, 2003, 06:03:32 ; Search time 6157 Seconds
(without alignments)
11211.930 Million cell updates/sec

Title: US-10-005-344-1
Perfect score: 2372
Sequence: 1 gcaaccgcgcgagcttgctg.....attacagcgatgagccacgc 2372

Scoring table: OLIGO.NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 995600

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb_ba.*
- 2: gb_hgt.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
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- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
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- 31: em_hgt_inv.*
- 32: em_hgt_other.*
- 33: em_hgt_mus.*
- 34: em_hgt_pln.*
- 35: em_hgt_rod.*
- 36: em_hgt_mam.*
- 37: em_hgt_vit.*
- 38: em_sy.*
- 39: em_hgt_hum.*
- 40: em_hgt_mus.*
- 41: em_hgtg_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

✓ *length of region of 100% matches*

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	2.0	90	9	HUMDLRFL
2	43	1.8	80	9	HUMBRKFA
3	43	1.8	92	6	AX197472
4	39	1.6	80	9	HUMBRKFA
5	39	1.6	85	6	AR051522
6	39	1.6	85	6	AR072662
7	39	1.6	85	6	AR073207
8	38	1.6	80	9	HUMBRKFA
9	37	1.6	51	6	AX158065
10	37	1.6	51	6	AX161490
11	37	1.6	51	6	AX163420
12	37	1.6	90	9	HUMDLRFL
13	37	1.6	94	6	AX197487
14	36	1.5	51	6	AX161652
15	36	1.5	76	6	A97233
16	35	1.5	40	6	AR208401
17	35	1.5	51	6	AX163202
18	35	1.5	70	9	HSLAS32
19	34	1.4	51	6	AX158807
20	34	1.4	51	6	AX161913
21	34	1.4	54	6	AX322189
22	32	1.3	51	6	AX157145
23	32	1.3	51	6	AX160937
24	32	1.3	92	6	AX197468
25	32	1.3	94	6	AX197476
26	32	1.3	94	6	AX197483
27	31	1.3	66	9	AF087511
28	30	1.3	40	6	A68621
29	30	1.3	51	6	AX156918
30	30	1.3	51	6	AX158063
31	30	1.3	51	6	AX159155
32	30	1.3	51	6	AX190033
33	30	1.3	51	9	S62605
34	30	1.3	100	9	HSU67848
35	29	1.2	29	6	AR208404
36	29	1.2	51	6	AX118161
37	29	1.2	51	6	AX163193
38	29	1.2	51	6	AX163312
39	29	1.2	60	6	AR051487
40	29	1.2	60	6	AR072627
41	29	1.2	60	6	AR073172
42	29	1.2	76	6	AR051499
43	29	1.2	76	6	AR072639
44	29	1.2	76	6	AR073184
45	29	1.2	88	11	HUMUT5056B

ALIGNMENTS

RESULT 1
HUMDLRFL
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

HUMDLRFL 90 bp DNA linear PRI 11-JAN-1995
Human low density lipoprotein receptor intron A Alu repeat.
K03555
K03555.1 GI:187104
Alu repeat; low density lipoprotein receptor-1; repeat region.
Human DNA.
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 90)
Lehrman, M.A., Goldstein, J.L., Russell, D.W. and Brown, M.S.
Duplication of seven exons in LDL receptor gene caused by Alu-Alu
recombination in a subject with familial hypercholesterolemia

JOURNAL Cell 48 (5), 827-835 (1987)
 MEDLINE 87131094
 PUBMED 3815525
 COMMENT Clean copy of sequence kindly provided by M.Lehrman (22-APR-1987).
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 Location/Qualifiers
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 /organism="Homo sapiens"
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 /map="19p13.3"
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 /gene="LDLR"
 /note="hqlm; G00-119-362"
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 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2325 GCCCAGCTCGGCTCCCAAGTCTGGATTACAGGCATGAGCCACC 2371
 Db 33 GCCCAGCTCGGCTCCCAAGTCTGGATTACAGGCATGAGCCACC 79
 RESULT 2
 HUMBRKFCAC Human alpha-galactosidase breakpoint region. 80 bp DNA linear PRI 27-APR-1993
 LOCUS
 DEFINITION
 ACCESSION M36133
 VERSION M36133.1 GI:179543
 KEYWORDS Fabry disease; breakpoint junction; glycosphingolipid catabolism.
 SOURCE Human DNA.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 80).
 AUTHORS Kornreich, R., Bishop, D.F. and Desnick, R.J.
 TITLE Alpha-galactosidase A gene rearrangements causing Fabry disease.
 Identification of short direct repeats at breakpoints in an
 Alu-rich gene
 JOURNAL J. Biol. Chem. 265 (16), 9319-9326 (1990)
 MEDLINE 90264427
 PUBMED 2160973
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 18 a 28 c 17 g 17 t
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 Best Local Similarity 100.0%; Pred. No. 1.7e-11;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2330 CTTGGCTCCCAAGTCTGGATTACAGGCATGAGCCACC 2372
 Db 17 CTTGGCTCCCAAGTCTGGATTACAGGCATGAGCCACC 59
 RESULT 3
 AX197472/c
 LOCUS AX197472 92 bp DNA linear PAT 29-AUG-2001
 DEFINITION Sequence 37 from Patent WO0151632.
 ACCESSION AX197472
 VERSION AX197472.1 GI:15387842
 KEYWORDS human.
 SOURCE Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 92)
 AUTHORS padigar, M., Prayaga, S.K., Taupier, R.J., Mishra, V., Tchernev, V.T.,
 Spytek, K.A. and Li, L.

TITLE
 JOURNAL
 Patent: WO 0151632-A 37 19-JUL-2001;
 Curagen Corporation (US)
 FEATURES
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 Location/Qualifiers
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
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 Best Local Similarity 100.0%; Pred. No. 1.6e-11;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2319 TGATCGCCGACCTCGGCTCCCAAGTCTGGATTACAGGC 2361
 Db 59 TGATCGCCGACCTCGGCTCCCAAGTCTGGATTACAGGC 17
 RESULT 4
 HUMBRKFAB Human alpha-galactosidase breakpoint family F. 80 bp DNA linear PRI 27-APR-1993
 LOCUS
 DEFINITION
 ACCESSION M36132
 VERSION M36132.1 GI:179542
 KEYWORDS Fabry disease; breakpoint junction; glycosphingolipid catabolism.
 SOURCE Human DNA.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 80)
 AUTHORS Kornreich, R., Bishop, D.F. and Desnick, R.J.
 TITLE Alpha-galactosidase A gene rearrangements causing Fabry disease.
 Identification of short direct repeats at breakpoints in an
 Alu-rich gene
 JOURNAL J. Biol. Chem. 265 (16), 9319-9326 (1990)
 MEDLINE 90264427
 PUBMED 2160973
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 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2334 GGCCTCCCAAGTCTGGATTACAGGCATGAGCCACC 2372
 Db 21 GGCCTCCCAAGTCTGGATTACAGGCATGAGCCACC 59
 RESULT 5
 AR051522
 LOCUS AR051522 85 bp DNA linear PAT 29-SEP-1999
 DEFINITION Sequence 92 from patent US 5830670.
 ACCESSION AR051522
 VERSION AR051522.1 GI:5974886
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 85)
 AUTHORS de la Monte, S. and Wands, J.R.
 TITLE Neural thread protein gene expression and detection of Alzheimer's disease
 Patent: US 5830670-A 92 03-NOV-1998;
 JOURNAL Location/Qualifiers
 FEATURES
 source
 Location/Qualifiers
 1..85
 /organism="unknown"
 BASE COUNT 13 a 27 c 25 g 20 t

ORIGIN

Query Match 1.6%; Score 39; DB 6; Length 85;
Best Local Similarity 100.0%; Pred. No. 2.6e-09;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2290 GCCAGGATGTCGATCTCCTGACCTCGTGATCGGCC 2328
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Db 9 GCCAGGATGTCGATCTCCTGACCTCGTGATCGGCC 47
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RESULT 6
AR072662

LOCUS AR072662 85 bp DNA linear PAT 28-AUG-2000

DEFINITION Sequence 92 from patent US 5948634.

ACCESSION AR072662

VERSION AR072662.1 GI:9999426

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 85)

AUTHORS de la Monte,S. and Wands,J.R.

TITLE Neural Thread protein gene expression and detection of alzheimer's disease

JOURNAL Patent: US 5948634-A 92 07-SEP-1999;

FEATURES Location/Qualifiers

source 1..85

BASE COUNT 13 a 27 c 25 g 20 t

ORIGIN

Query Match 1.6%; Score 39; DB 6; Length 85;
Best Local Similarity 100.0%; Pred. No. 2.6e-09;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2290 GCCAGGATGTCGATCTCCTGACCTCGTGATCGGCC 2328
|||||
Db 9 GCCAGGATGTCGATCTCCTGACCTCGTGATCGGCC 47
|||||

RESULT 7
AR073207

LOCUS AR073207 85 bp DNA linear PAT 28-AUG-2000

DEFINITION Sequence 92 from patent US 5948888.

ACCESSION AR073207

VERSION AR073207.1 GI:9999970

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 85)

AUTHORS de la Monte,S. and Wands,J.R.

TITLE Neural Thread protein gene expression and detection of Alzheimer's disease

JOURNAL Patent: US 5948888-A 92 07-SEP-1999;

FEATURES Location/Qualifiers

source 1..85

BASE COUNT 13 a 27 c 25 g 20 t

ORIGIN

Query Match 1.6%; Score 39; DB 6; Length 85;
Best Local Similarity 100.0%; Pred. No. 2.6e-09;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2290 GCCAGGATGTCGATCTCCTGACCTCGTGATCGGCC 2328
|||||
Db 9 GCCAGGATGTCGATCTCCTGACCTCGTGATCGGCC 47
|||||

RESULT 8
HUMBRKFAA

LOCUS HUMBRKFAA 80 bp DNA linear PRI 27-APR-1993

DEFINITION Human alpha-galactosidase breakpoint region.

ACCESSION M36131

VERSION M36131.1 GI:179541

KEYWORDS Fabry disease; breakpoint junction; glycosphingolipid catabolism.

SOURCE Human DNA.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Kornreich,R., Bishop,D.F. and Desnick,R.J.

TITLE Alpha-galactosidase A gene rearrangements causing Fabry disease. Identification of short direct repeats at breakpoints in an Alu-rich gene

JOURNAL J. Biol. Chem. 265 (16), 9319-9326 (1990)

MEDLINE 90264427

PUBMED 2160973

FEATURES Location/Qualifiers

source 1..80

BASE COUNT 19 a 28 c 20 g 13 t

ORIGIN

Query Match 1.6%; Score 38; DB 9; Length 80;
Best Local Similarity 100.0%; Pred. No. 9e-09;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2334 GGCCTCCCAAGTCTGGGATTACAGCATGCCACC 2371
|||||
Db 21 GGCCTCCCAAGTCTGGGATTACAGCATGCCACC 58
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RESULT 9
AX158065

LOCUS AX158065 51 bp DNA linear PAT 22-JUN-2001

DEFINITION Sequence 1393 from Patent WO0140521.

ACCESSION AX158065

VERSION AX158065.1 GI:14539396

KEYWORDS human.

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Shimkets,R.A. and Leach,M.

TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof

JOURNAL Patent: WO 0140521-A 1393 07-JUN-2001;

FEATURES Location/Qualifiers

source 1..51

BASE COUNT 9 a 21 c 12 g 9 t

ORIGIN

Query Match 1.6%; Score 37; DB 6; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.3e-08;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2318 GTGATCCGCCACCTCGGCTCCCAAGTCTGGAT 2354
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Db 15 GTGATCCGCCACCTCGGCTCCCAAGTCTGGAT 51
|||||

RESULT 10
AX161490

LOCUS AX161490 51 bp DNA linear PAT 22-JUN-2001

DEFINITION Sequence 4818 from Patent WO0140521.

ACCESSION AX161490
VERSION AX161490.1 GI:14542821
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 51)
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 4818 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
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/db_xref="taxon:9606"
misc_feature 26
/note="2 of 2 allelic variants (4817 is other entry)"
BASE COUNT 7 a 22 c 11 g 11 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 3.3e-08;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2292 CAGGATGCTCTCGATCTCCTGACCTCGTGATCGGCC 2328
|||||
Db 1 CAGGATGCTCTCGATCTCCTGACCTCGTGATCGGCC 37
|||||
RESULT 11
AX163420/c
LOCUS AX163420 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 6748 from Patent WO0140521.
ACCESSION AX163420
VERSION AX163420.1 GI:14544751
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 51)
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 6748 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
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/db_xref="taxon:9606"
misc_feature 26
/note="2 of 2 allelic variants (6747 is other entry)"
BASE COUNT 10 a 12 c 20 g 9 t
ORIGIN
Query Match 1.6%; Score 37; DB 6; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.3e-08;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2318 GGGATCCGCCACCTCGGCCCTCCCAAGTCTGGGAT 2354
|||||
Db 37 GGGATCCGCCACCTCGGCCCTCCCAAGTCTGGGAT 1
|||||
RESULT 12
HUMLDLRM
LOCUS HUMLDLRM 90 bp DNA linear PRI 11-JAN-1995
DEFINITION Human low density lipoprotein receptor mutant gene recombination
site.

ACCESSION M15365
VERSION M15365.1 GI:187107
KEYWORDS Alu repeat; LDL receptor; cell surface protein; crossover;
recombination.
SOURCE Human (FH 295) fibroblast DNA, clone p295.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 90)
AUTHORS Lehman,M.A., Goldstein,J.L., Russell,D.W. and Brown,M.S.
TITLE Duplication of seven exons in LDL receptor gene caused by Alu-Alu
recombination in a subject with familial hypercholesterolemia
JOURNAL Cell 48 (5), 827-835 (1987)
MEDLINE 87131094
PUBMED 3815525
COMMENT Clean copy of sequence kindly provided by M.Lehman (22-APR-1987).
Individual FH 295 carries two mutant LDL receptor alleles. The
allele below was inherited from the father and includes a
duplication of exons 2 through 8 that was presumably created by
unequal chromosomal crossover involving Alu repeats in introns 1
and 8. The exact site of recombination cannot be determined
because the sequences of the Alu repeats in introns 1 and 8 of
normal alleles are identical over a span of 26 nucleotides at the
recombination site.
FEATURES
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/note="LDLR Intron 8; G00-119-362"
43..68
/organism="Homo sapiens"
68..>90
/note="LDLR duplicated intron 1 (no splice consensus at
68); putative; does not fit consensus"
BASE COUNT 18 a 33 c 19 g 20 t
ORIGIN 1 bp upstream of NheI site; chromosome 19p13.2-p13.1.
Query Match 1.6%; Score 37; DB 9; Length 90;
Best Local Similarity 100.0%; Pred. No. 3.2e-08;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2335 GCCTCCCAAGTCTGGGATTACAGGCATGAGCCACC 2371
|||||
Db 43 GCCTCCCAAGTCTGGGATTACAGGCATGAGCCACC 79
|||||
RESULT 13
AX197487
LOCUS AX197487 94 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 52 from Patent WO0151632.
ACCESSION AX197487
VERSION AX197487.1 GI:15387847
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 94)
AUTHORS Padigaru,M., Prayaga,S.K., Taupier,R.J., Mishra,V., Tchernev,V.T.,
Spytek,K.A. and Li,L.
TITLE Odorant receptor polypeptides and nucleic acids encoding same
JOURNAL Patent: WO 0151632-A 52 19-JUL-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
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BASE COUNT 16 a 31 c 26 g 21 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3.1e-08;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2334 GCCCTCCCAAGTCTGGGATTACAGCATGAGCCAC 2370
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Db 49 GGCCTCCCAAGTCTGGGATTACAGCATGAGCCAC 85

RESULT 14

AX161652/c AX161652 51 bp DNA linear PAT 22-JUN-2001
LOCUS
DEFINITION Sequence 4980 from Patent WO0140521.
ACCESSION AX161652
VERSION AX161652.1 GI:14542983
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Shimkets, R.A. and Leach, M.
Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof

JOURNAL Patent: WO 0140521-A 4980 07-JUN-2001;
Curagen Corporation (US)

FEATURES
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Location/Qualifiers
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Accession number C943979411"

BASE COUNT 10 a 13 c 17 g 11 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2335 GCCCTCCCAAGTCTGGGATTACAGCATGAGCCAC 2370
|||||
Db 41 GGCCTCCCAAGTCTGGGATTACAGCATGAGCCAC 6

RESULT 15

A97233 A97233 76 bp DNA linear PAT 26-JAN-2000
LOCUS
DEFINITION Sequence 79 from Patent WO9918235.
ACCESSION A97233
VERSION A97233.1 GI:6780621
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified

REFERENCE 1 (bases 1 to 76)
AUTHORS Abken, H.

TITLE PROCESS FOR DETECTING, EXTRACTING OR REMOVING HUMAN OR MAMMALIAN
CELLS WITH A DISTURBED CELLULAR CYCLE REGULATION OR UNLIMITED
PROLIFERATION OR TUMOUR-FORMING ABILITY

JOURNAL Patent: WO 9918235-A 79 15-APR-1999;
ABKEN HINRICH (DE)

FEATURES
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.1e-07;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2325 GCCCACCCTCGGCTTCCCAAGTCTGGGATTACAGG 2360
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Db 6 GCCCACCCTCGGCTTCCCAAGTCTGGGATTACAGG 41

Search completed: January 11, 2003, 08:55:30
Job time : 6160 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 11, 2003, 03:27:22 ; Search time 490 Seconds
(without alignments)
10901.510 Million cell updates/sec

Title: US-10-005-344-1
Perfect score: 2372
Sequence: 1 gcacgcgcgacttgctg.....attacagcagcagccaccg 2372

Scoring table: OLIGO_NUC
Gapop 60.0 , Capext 60.0

Searched: 2185239 seqs, 112599159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2390332

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
c 1	73	3.1	73	AA35141	Nucleotide sequence
2	60	2.5	60	ABN19842	Human spliced tran
3	50	2.1	95	AA28711	Human secreted pro
4	47	2.0	47	AA269526	Human map-related
c 5	46	1.9	95	AAK85116	Human immune/haema
c 6	44	1.9	76	AAK13689	Human secreted pro.
c 7	42	1.8	87	AA137410	Human musculoskele
8	42	1.8	100	ABA20222	Human nervous syst
c 9	41	1.7	86	AAK14994	Human secreted pro

10	40	1.7	99	22	AAK83535	Human immune/haema
11	40	1.7	99	22	AAK86591	Human immune/haema
c 12	39	1.6	99	21	AAK14830	Human secreted pro
c 13	38	1.6	67	21	AAK14689	Human secreted pro
c 14	38	1.6	79	21	AAK24033	Human secreted pro
c 15	38	1.6	98	22	AAK85113	Human immune/haema
c 16	37	1.6	51	21	AAK77228	Human clone Cg4397
17	37	1.6	51	22	AAI74452	Human silent SNP c
18	37	1.6	51	22	AAI77877	Human silent SNP c
c 19	37	1.6	51	22	AAI79807	Human nonconservat
c 20	37	1.6	57	22	AAK83961	Human immune/haema
c 21	37	1.6	84	21	AAK12517	Human secreted pro
c 22	37	1.6	88	22	AAK86579	Human immune/haema
c 23	37	1.6	91	22	AAK84173	Human immune/haema
c 24	36	1.5	51	21	AAK77000	Human clone Cg4294
c 25	36	1.5	51	22	AAI78039	Human silent SNP c
c 26	36	1.5	76	20	AAK37046	Human cdc37 nuclei
c 27	36	1.5	87	22	AAK87262	Human immune/haema
c 28	36	1.5	87	22	AAK87263	Human immune/haema
c 29	36	1.5	100	22	AAK03022	Human reproductive
c 30	36	1.5	100	22	AAK73008	Human immune/haema
c 31	35	1.5	40	21	AAK97659	Human MDM2 40mer P
c 32	35	1.5	40	24	ABL60505	Human MDM2 mRNA fr
c 33	35	1.5	51	22	AAI79589	Human silent SNP c
c 34	35	1.5	87	22	AAK76817	Human immune/haema
c 35	35	1.5	100	22	AAK90852	Human digestive sy
c 36	34	1.4	51	22	AAI75194	Human silent SNP c
c 37	34	1.4	51	22	AAI78300	Human silent SNP c
c 38	34	1.4	54	24	AAI68926	Activated T-cell d
c 39	34	1.4	65	21	AAK12925	Human secreted pro
c 40	33	1.4	51	22	AAK32116	Human SNP oligonuc
c 41	32	1.3	51	21	AAK77488	Human Alu subfamil
c 42	32	1.3	51	22	AAI73532	Human silent SNP c
c 43	32	1.3	51	22	AAI77324	Human silent SNP c
c 44	32	1.3	78	21	AAK11974	Human secreted pro
c 45	32	1.3	79	21	AAK12191	Human secreted pro

ALIGNMENTS

RESULT 1
AAK35141/c
ID AAK35141 standard; DNA; 73 BP.
XX AC AAK35141;
XX DT 01-JUL-1999 (first entry)
XX DE Nucleotide sequence SEQ ID 49.
XX KW MDM2 protein; antisense oligonucleotide; activator; tumour suppressor;
XX KW inhibition; tumour growth; DNA-damaging agent; camptothecin;
XX KW DNA/RNA hybrid; ss.
XX OS Synthetic.
XX PN WO9910486-A2.
XX PD 04-MAR-1999.
XX PF 18-AUG-1998; 98WO-US17147.
XX PR 06-MAY-1998; 98US-0073567.
XX PR 22-AUG-1997; 97US-0916384.
XX (HYBR-) HYBRIDON INC.
XX AG Agrawal S, Chen J, Zhang R;
XX WPI; 1999-254219/21.
XX PT New MDM2-specific antisense oligonucleotides

```
xx Disclosure; Page 57; 59pp; English.
xx
xx The specification describes antisense oligonucleotides that
xx inhibits MDM2 protein expression. The antisense oligonucleotides can
xx be used to activate a tumour suppressor. The antisense oligonucleotides
xx are used to inhibit tumour growth in a mammal, including a human,
xx particularly in conjunction with a DNA-damaging agent such as
xx camptothecin. The present sequence appears in the specification.
xx
xx Sequence 73 BP; 17 A; 23 C; 11 G; 22 T; 0 other;
xx
Query Match          3.1%; Score 73; DB 20; Length 73;
Best Local Similarity 100.0%; Pred. NO. 5e-25;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 73 AGGTACATCTGTGAGTGAACAGGTGTACCTTGAAGTGGGAGTGATCAAAAGGACCT 14
Qy 725 TGTACAGAGCTT 737
Db 13 TGTACAGAGCTT 1
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ID ABN39842 standard; DNA; 60 BP.
XX
AC ABN39842;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:12590.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Homo sapiens.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-IB01903.
XX
PR 28-JUL-2000; 2000US-221607P.
XX
PR 02-MAY-2001; 2001US-287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
WPI; 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes -
XX
PS Example 1; SEQ ID 12590; 47pp; English.
XX
XX The present invention describes oligonucleotide libraries for detecting
XX messenger RNAs that populate a (sub-)transcriptome, where the
XX (sub-)transcriptome comprises messenger RNAs transcribed from multiple
XX transcription units that populate a genome. The library comprises
XX several oligonucleotides, each capable of hybridising selectively to a
XX set of messenger RNAs transcribed from a given transcription unit of
XX the genome, which encodes one or more messenger RNA splice variants.
XX The oligonucleotide libraries are useful for detecting mRNAs from a
XX biological sample, in expression profiling studies, in qualitatively or
XX quantitatively characterising the corresponding transcriptome, and in
XX detecting RNA transcripts and splice variants of human or animal
CC transcriptsomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 60 BP; 10 A; 21 C; 16 G; 13 T; 0 other;
XX
Query Match          2.5%; Score 60; DB 24; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.1e-18;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 98 TGACCGAGATCCTGCTGCTTTTCGACGAGCAGGACCGTCCCTCCCGGATTAGTGCCTA 157
Db 1 TGACCGAGATCCTGCTGCTTTTCGACGAGCAGGACCGTCCCTCCCGGATTAGTGCCTA 60
RESULT 3
AAC28711
ID AAC28711 standard; cDNA; 95 BP.
XX
AC AAC28711;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein 5' EST, SEQ ID NO: 32786.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
XX
OS Homo sapiens.
XX
PN EP1033401-A2.
XX
PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-0200610.
XX
PR 26-FEB-1999; 99US-0122487.
XX
PA (GEST ) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX
WPI; 2000-500381/45.
XX
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
PS Claim 1; SEQ ID 32786; 71pp + CD-ROM; English.
XX
XX The present sequence is one of a large number of 5' ESTs derived from
XX mRNAs encoding secreted proteins. NO ORF has yet been conclusively
XX identified within the present sequence. The 5' ESTs were prepared from
XX total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
XX sequences usually correspond mainly to the 3' untranslated region (UTR)
XX of the mRNA because they are often obtained from oligo-dT primed cDNA
XX libraries. Such ESTs are not well suited for isolating cDNA sequences
XX derived from the 5' ends of mRNAs and even in those cases where longer
XX cDNA sequences have been obtained, the full 5' UTR is rarely included.
XX 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
XX used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
XX in diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX They are used to obtain upstream regulatory sequences and to design
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PR 06-SEP-2000; 2000US-0230437.
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PR 08-SEP-2000; 2000US-0231242.
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PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232297.
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PR 20-OCT-2000; 2000US-0240360.
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PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 06-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
Rosen CA, Barash SC, Ruben SM;
PI
XX WPI; 2001-483426/52.
DR
XX
PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
PS Disclosure; SEQ ID NO 39928; 3071pp + Sequence Listing; English.
XX
CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAK62170 to AAK61921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent
CC cancers and cancer metastases of haematopoietic-related diseases, especially
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 95 BP; 19 A; 26 C; 33 G; 17 T; 0 other;
Query Match 1.9%; Score 46; DB 22; Length 95;
Best Local Similarity 100.0%; Pred. No. 6.9e-12;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2327 CCACCTCGGGCTCCCAAAGTCTGGGATTACAGGCATGAGCCACCG 2372
|||||
Db 54 CCACCTCGGGCTCCCAAAGTCTGGGATTACAGGCATGAGCCACCG 9
RESULT 6
AAC13689/c
ID AAC13689 standard; cDNA; 76 BP.
XX
AC AAC13689;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein 5' EST, SEQ ID NO: 17764.
XX
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KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
OS Homo sapiens.
XX
XX
PN EPI033401-A2.
XX
XX
PD 06-SEP-2000.
XX
XX
PF 21-FEB-2000; 2000EP-0200610.
XX
XX
PR 26-FEB-1999; 99US-0122487.
XX
XX
FA (GSEST ) GENSET.
XX
XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX
XX
DR WPI; 2000-500381/45.
XX
XX
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
XX
PS Claim 1; SEQ ID 17764; 71pp + CD-ROM; English.
XX
XX
CC The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors.
XX
XX
SQ Sequence 76 BP; 19 A; 19 C; 25 G; 13 T; 0 other;

Query Match 1.9%; Score 44; DB 21; Length 76;
Best Local Similarity 100.0%; Pred. No. 6.5e-11;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2285 TGTTAGCCAGGATGCTCGATCCCTGACCTCGTATCGGCC 2328
DB 76 TGTTAGCCAGGATGCTCGATCCCTGACCTCGTATCGGCC 33

RESULT 7
AAL37410/c
ID AAL37410 standard; DNA; 87 BP.
XX
XX
AC AAL37410;
XX
XX
DT 08-JAN-2002 (first entry)
XX
XX
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3775.
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;
KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein;
KW musculoskeletal system; ds.
OS Homo sapiens.
XX
XX
PN WO200155367-A1.
XX
XX
PD 02-AUG-2001.
XX
XX
PR 17-JAN-2001; 2001WO-US01338.
XX
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184564.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
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PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
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PR 14-AUG-2000; 2000US-0225447.
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PR 18-AUG-2000; 2000US-0226279.
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PR 23-AUG-2000; 2000US-0227009.
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PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
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PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
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PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
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PR 26-SEP-2000; 2000US-0235484.
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PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
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PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241026.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
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PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
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PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
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PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
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PR 17-NOV-2000; 2000US-0249211.
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PR 17-NOV-2000; 2000US-0249213.
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PR 17-NOV-2000; 2000US-0249216.
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PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249219.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
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PR 17-NOV-2000; 2000US-0249299.
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PR 01-DEC-2000; 2000US-0250160.
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PR 05-DEC-2000; 2000US-0251030.
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PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-451937/48.
XX

PT Isolated polypeptide for treating, preventing and/or prognosing
PT disorders related to the musculoskeletal system including
PT musculoskeletal cancers and also for testing and detection e.g.
PT diagnosis -
XX
PS Example 2; SEQ ID NO 3775; 781pp + Sequence Listing; English.
XX
CC The invention relates to novel genes (AAL34669-AAL37666) and proteins
CC (AB03087-AB04109) associated with the musculoskeletal system useful
CC for preventing, treating or ameliorating medical conditions e.g. by
CC protein or gene therapy. The genes are isolated from a range of human
CC tissues disclosed in the specification. The nucleic acids, proteins,
CC antibodies and (ant)agonists are useful in the diagnosis, treatment
CC and prevention of: (a) cancer, e.g. breast and ovarian cancer and
CC other cancers of the adrenal gland, bone, bone marrow, breast,
CC gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
CC (c) cardiovascular disorders such as myocardial ischaemia; (d) wound
CC healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy;
CC and (f) infectious diseases such as viral, bacterial, fungal and
CC parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 87 BP; 19 A; 23 C; 29 G; 16 T; 0 other;

Query Match 1.8%; Score 42; DB 22; Length 87;
Best Local Similarity 100.0%; Pred. No. 6.1e-10;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2319 TGATCGCCACCTCGGCTCCAAAGTCTGGGATTACAG 2360
DB 48 TGATCGCCACCTCGGCTCCAAAGTCTGGGATTACAG 7

RESULT 8
ABA20222
ID ABA20222 standard; DNA; 100 BP.
XX
XX ABA20222;
AC ABA20222;
XX
DT 23-JAN-2002 (first entry)
XX
DE Human nervous system related polynucleotide SEQ ID NO 12553.
XX
KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnary;
KW antiparkinsonian; antischizoid; antianaemic; antiarthritic; cancer;
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
XX
OS Homo sapiens.
XX
XX WO200159063-A2.
XX
XX 16-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US01334.
XX
XX 31-JAN-2000; 2000US-0179065.
XX 04-FEB-2000; 2000US-0180628.
XX 24-FEB-2000; 2000US-0184664.
XX 02-MAR-2000; 2000US-0186350.
XX 16-MAR-2000; 2000US-0189874.
XX 17-MAR-2000; 2000US-0190076.
XX 18-APR-2000; 2000US-0198123.
XX 19-MAY-2000; 2000US-0205515.
XX 07-JUN-2000; 2000US-0209467.

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PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
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PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
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PR 30-AUG-2000; 2000US-0228924.
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PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
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PR 26-SEP-2000; 2000US-0235484.
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PR 27-SEP-2000; 2000US-0235836.
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PR 02-OCT-2000; 2000US-0236370.
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PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
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PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
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PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 20-OCT-2000; 2000US-0242221.
PR 01-NOV-2000; 2000US-0244517.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
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PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
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PR 08-NOV-2000; 2000US-0246609.
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PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
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PR 17-NOV-2000; 2000US-0249211.
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PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250391.
PR 01-DEC-2000; 2000US-0251160.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-541565/60.
XX
XX Nucleic acids encoding 3224 human nervous system antigen polypeptides,
PT useful for preventing, diagnosing and/or treating nervous system
PT cancers and metastases -
XX
XX Disclosure; SEQ ID NO 12553; 1701pp + Sequence Listing; English.
PS
XX The invention relates to novel genes (AB11004-ABA21534) and proteins
CC (AB114678-AB18001) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast

CC and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 100 BP; 22 A; 30 C; 26 G; 22 T; 0 other;

Query Watch 1.8%; Score 42; DB 22; Length 100;
Best Local Similarity 100.0%; Pred. No. 6.1e-10;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2325 GCCCACTCGGCTCCCAAAGTGGATTACAGGCATGAG 2366
| | | | | | | | | | | | | | | | | | | | | |
DB 59 GCCCACTCGGCTCCCAAAGTGGATTACAGGCATGAG 100

RESULT 9
AACI4994/c
ID AACI4994 standard; cDNA; 86 BP.
AC AACI4994;
XX
XX DT 06-OCT-2000 (first entry)
XX
XX Human secreted protein 5' EST, SEQ ID NO: 19069.
XX
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
XX Homo sapiens.
OS
PN EP1033401-A2.
PP
PD 06-SEP-2000.
XX
XX 21-FEB-2000; 2000EP-0200610.
XX
XX 26-FEB-1999; 99US-0122487.
XX
XX (GEST) GENSET.
PA
PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX
XX WPI; 2000-500381/45.
XX
XX
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
XX Claim 1; SEQ ID 19069; 7lpp + CD-ROM; English.
PS
XX
XX The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors.

[illegible]

05-SEP-2000; 2000US-02239509.	PR	17-NOV-2000; 2000US-0249216.	PR
05-SEP-2000; 2000US-02239513.	PR	17-NOV-2000; 2000US-0249217.	PR
06-SEP-2000; 2000US-0230437.	PR	17-NOV-2000; 2000US-0249218.	PR
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08-SEP-2000; 2000US-0232080.	PR	17-NOV-2000; 2000US-0249300.	PR
08-SEP-2000; 2000US-0232081.	PR	01-DEC-2000; 2000US-0250160.	PR
12-SEP-2000; 2000US-0231968.	PR	01-DEC-2000; 2000US-0250391.	PR
14-SEP-2000; 2000US-0232397.	PR	05-DEC-2000; 2000US-0251030.	PR
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21-SEP-2000; 2000US-0234274.	PR	11-DEC-2000; 2000US-0254097.	PR
25-SEP-2000; 2000US-0234997.	PR	05-JAN-2001; 2001US-02559678.	PR
25-SEP-2000; 2000US-0234998.	PR		XX
25-SEP-2000; 2000US-0234984.	PR	(HUMA-) HUMAN GENOME SCI INC.	PA
27-SEP-2000; 2000US-0233634.	PR		XX
27-SEP-2000; 2000US-0233636.	PR	Rosen CA, Barash SC, Ruben SM;	PI
29-SEP-2000; 2000US-0236327.	PR	WPI; 2001-483426/52.	XX
29-SEP-2000; 2000US-0236367.	PR		XX
29-SEP-2000; 2000US-0236368.	PR		XX
29-SEP-2000; 2000US-0236369.	PR	Nucleic acids encoding human immune/hematopoietic antigen polypeptides,	PT
29-SEP-2000; 2000US-0236370.	PR	useful for preventing, diagnosing and/or treating cancers and	PT
02-OCT-2000; 2000US-0236802.	PR	metastasis -	PT
02-OCT-2000; 2000US-0237037.	PR		XX
02-OCT-2000; 2000US-0237038.	PR	Disclosure; SEQ ID NO 38347; 3071pp + Sequence Listing; English.	PS
02-OCT-2000; 2000US-0237039.	PR		XX
02-OCT-2000; 2000US-0237040.	PR	AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)	CC
13-OCT-2000; 2000US-0239935.	PR	amino acid sequences given in AAK821170 to AAK91921. (I) have cytostatic	CC
13-OCT-2000; 2000US-0239937.	PR	activity, and can be used in gene therapy and vaccine production. (I)	CC
20-OCT-2000; 2000US-0240960.	PR	proteins and polynucleotides may be used in the prevention, diagnosis and	CC
20-OCT-2000; 2000US-0241221.	PR	treatment of diseases associated with inappropriate (I) expression. For	CC
20-OCT-2000; 2000US-0241785.	PR	example, they may be used to treat disorders associated with decreased	CC
20-OCT-2000; 2000US-0241786.	PR	expression by rectifying mutations or deletions in a patient's genome	CC
20-OCT-2000; 2000US-0241787.	PR	that affect the activity of (I) by expressing inactive proteins or to	CC
20-OCT-2000; 2000US-0241808.	PR	supplement the patients own production of (I). Additionally, (I)	CC
20-OCT-2000; 2000US-0241809.	PR	the nucleic acids into a host cell and culturing the cell to express the	CC
20-OCT-2000; 2000US-0241826.	PR	polynucleotides may be used to produce the secreted (I), by inserting	CC
01-NOV-2000; 2000US-0244617.	PR	the nucleic acids into a host cell and culturing the cell to express the	CC
08-NOV-2000; 2000US-0246474.	PR	protein. (I) proteins and polynucleotides may be used to prevent,	CC
08-NOV-2000; 2000US-0246475.	PR	diagnose and treat immune/haematopoietic-related diseases, especially	CC
08-NOV-2000; 2000US-0246476.	PR	cancers and cancer metastases of haematopoietic-derived cells. AAK64703	CC
08-NOV-2000; 2000US-0246477.	PR	to AAK87694 represent human immune/haematopoietic antigen genomic	CC
08-NOV-2000; 2000US-0246478.	PR	sequences from the present invention. AAK54942 to AAK54950 and AAK821169	CC
08-NOV-2000; 2000US-0246523.	PR	represent sequences used in the exemplification of the present invention.	CC
08-NOV-2000; 2000US-0246524.	PR		XX
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08-NOV-2000; 2000			

DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41403.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US01354.
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XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184654.
PR 02-MAR-2000; 2000US-0186350.
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PR 30-JUN-2000; 2000US-0215135.
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PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
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PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
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PR 14-SEP-2000; 2000US-0233065.
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PR 25-SEP-2000; 2000US-0234997.
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PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
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PR 02-OCT-2000; 2000US-0236802.
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PR 20-OCT-2000; 2000US-0240960.
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PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
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PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
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PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
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PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
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PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
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PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 03-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251869.
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PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and
XX metastasis -
XX
XX Disclosure: SEQ ID NO 41403; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
XX amino acid sequences given in AAM02170 to AAM91921. (I) have cytostatic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For
XX example, they may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of (I) by expressing inactive proteins or to
XX supplement the patient's own production of (I). Additionally, (I)
XX polynucleotides may be used to produce the secreted (I), by inserting
XX the nucleic acids into a host cell and culturing the cell to express the
XX protein. (I) proteins and polynucleotides may be used to prevent,
XX diagnose and treat immune/hematopoietic-related diseases, especially
XX cancers and cancer metastases of hematopoietic-derived cells. AAK64703
XX to AAK87694 represent human immune/hematopoietic antigen genomic
XX sequences from the present invention. AAK54942 to AAK54950 and AAM82169
XX represent sequences used in the exemplification of the present invention.
XX
XX Sequence 99 BP; 19 A; 33 C; 27 G; 20 T; 0 other;
SQ

Query Match 1.7%; Score 40; DB 22; Length 99;
Best Local Similarity 100.0%; Pred. No. 5.7e-09;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2330 CCTCGGCTCCCAAGTGTGGGATTACAGGCATGAGCCA 2369
|||||
DB 60 CCTCGGCTCCCAAGTGTGGGATTACAGGCATGAGCCA 99
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RESULT 12
AAC14830
ID AAC14830 standard; cDNA; 99 BP.
XX
XX AAC14830;
XX
XX 06-OCT-2000 (first entry)
XX Human secreted protein 5' EST, SEQ ID NO: 18905.
XX
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX gene therapy; chromosome mapping; ss.
XX Homo sapiens.
XX
XX EPI033401-A2.
XX
XX 06-SEP-2000.
XX
XX 21-FEB-2000; 2000EP-0200610.
XX
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX gene therapy; chromosome mapping; ss.
XX Homo sapiens.
XX
XX EPI033401-A2.
XX
XX 06-SEP-2000.
XX
XX 21-FEB-2000; 2000EP-0200610.
XX
XX 26-FEB-1999; 99US-0122487.
XX
XX (GSET) GENSET.
XX
XX Dumas Milne Edwards J, Duclert A, Giordano J;
XX WPI; 2000-500381/45.
XX

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
XX diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
XX Claim 1; SEQ ID 18905; 71pp + CD-ROM; English.
XX
XX The present sequence is one of a large number of 5' ESTs derived from
XX mRNAs encoding secreted proteins. No ORF has yet been conclusively
XX identified within the present sequence. The 5' ESTs were prepared from
XX total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
XX sequences usually correspond mainly to the 3' untranslated region (UTR)
XX of the mRNA because they are often obtained from oligo-dT primed cDNA
XX libraries. Such ESTs are not well suited for isolating cDNA sequences
XX derived from the 5' ends of mRNAs and even in those cases where longer
XX cDNA sequences have been obtained, the full 5' UTR is rarely included.
XX 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
XX used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
XX in diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX They are used to obtain upstream regulatory sequences and to design
XX expression and secretion vectors.
XX
XX Sequence 99 BP; 14 A; 33 C; 27 G; 25 T; 0 other;
SQ

Query Match 1.6%; Score 39; DB 21; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2334 GGCCTCCCAAGTGTGGGATTACAGGCATGAGCCACCG 2372
|||||
DB 50 GGCCTCCCAAGTGTGGGATTACAGGCATGAGCCACCG 88
|||||

RESULT 13
AAC14689/C
ID AAC14689 standard; cDNA; 67 BP.
XX
XX AAC14689;
XX
XX 06-OCT-2000 (first entry)
XX Human secreted protein 5' EST, SEQ ID NO: 18764.
XX
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX gene therapy; chromosome mapping; ss.
XX Homo sapiens.
XX
XX EPI033401-A2.
XX
XX 06-SEP-2000.
XX
XX 21-FEB-2000; 2000EP-0200610.
XX
XX 26-FEB-1999; 99US-0122487.
XX
XX (GSET) GENSET.
XX
XX Dumas Milne Edwards J, Duclert A, Giordano J;
XX WPI; 2000-500381/45.
XX
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
XX diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
XX Claim 1; SEQ ID 18764; 71pp + CD-ROM; English.
XX
XX The present sequence is one of a large number of 5' ESTs derived from
XX mRNAs encoding secreted proteins. No ORF has yet been conclusively
XX identified within the present sequence. The 5' ESTs were prepared from
XX total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
XX sequences usually correspond mainly to the 3' untranslated region (UTR)

CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors.

XX SQ Sequence 67 BP; 17 A; 11 C; 18 G; 21 T; 0 other;

Query Match 1.6%; Score 38; DB 21; Length 67;

Best Local Similarity 100.0%; Pred. No. 5.4e-08; Mismatches 0; Indels 0; Gaps 0;

XX QY 2328 CACCTCGGCTCCCAAGTGTGGATTACAGCATGA 2365

DB 66 CACCTCGGCTCCCAAGTGTGGATTACAGCATGA 29

RESULT 14

AAC24033

ID AAC24033 standard; cDNA; 79 BP.

XX AC AAC24033;

XX DT 06-OCT-2000 (first entry)

XX DE Human secreted protein 5' EST, SEQ ID NO: 28108.

XX KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX KW gene therapy; chromosome mapping; ss.

XX OS Homo sapiens.

XX PN EP1033401-A2.

XX PD 06-SEP-2000.

XX PF 21-FEB-2000; 2000EP-0200610.

XX PR 26-FEB-1999; 99US-0122487.

XX PA (GST) GENSET.

XX PI Dumas Milne Edwards J, Duclert A, Giordano J;

XX DR WPI; 2000-500381/45.

XX PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
XX PT diagnostic, forensic, gene therapy and chromosome mapping procedures -

XX PS Claim 1; SEQ ID 28108; 71pp + CD-ROM; English.

XX CC The present sequence is one of a large number of 5' ESTs derived from
XX CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
XX CC identified within the present sequence. The 5' ESTs were prepared from
XX CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
XX CC sequences usually correspond mainly to the 3' untranslated region (UTR)
XX CC of the mRNA because they are often obtained from oligo-dT primed cDNA
XX CC libraries. Such ESTs are not well suited for isolating cDNA sequences
XX CC derived from the 5' ends of mRNAs and even in those cases where longer
XX CC cDNA sequences have been obtained, the full 5' UTR is rarely included.

XX CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
XX CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
XX CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX CC They are used to obtain upstream regulatory sequences and to design
XX CC expression and secretion vectors.

XX SQ Sequence 79 BP; 14 A; 21 C; 18 G; 26 T; 0 other;

Query Match 1.6%; Score 38; DB 21; Length 79;

Best Local Similarity 100.0%; Pred. No. 5.4e-08; Mismatches 0; Indels 0; Gaps 0;

XX QY 2291 CCAGGATGCTCTCGATCTCCTGACCTCTGATCGGCC 2328

DB 40 CCAGGATGCTCTCGATCTCCTGACCTCTGATCGGCC 77

RESULT 15

AAK85113/c

ID AAK85113 standard; DNA; 98 BP.

XX AC AAK85113;

XX DT 07-NOV-2001 (first entry)

XX DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39925.

XX KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX KW cytostatic; gene therapy; vaccine; metastasis; ds.

XX OS Homo sapiens.

XX PN WO200157182-A2.

XX PD 09-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US01354.

XX PR 31-JAN-2000; 2000US-0179065.

XX PR 04-FEB-2000; 2000US-0180628.

XX PR 24-FEB-2000; 2000US-0184664.

XX PR 02-MAR-2000; 2000US-0186350.

XX PR 16-MAR-2000; 2000US-0189874.

XX PR 17-MAR-2000; 2000US-0190076.

XX PR 18-APR-2000; 2000US-0198123.

XX PR 19-MAY-2000; 2000US-0205515.

XX PR 07-JUN-2000; 2000US-0209467.

XX PR 28-JUN-2000; 2000US-0214886.

XX PR 30-JUN-2000; 2000US-0215135.

XX PR 07-JUL-2000; 2000US-0216647.

XX PR 11-JUL-2000; 2000US-0217487.

XX PR 14-JUL-2000; 2000US-0217496.

XX PR 26-JUL-2000; 2000US-0220963.

XX PR 14-AUG-2000; 2000US-0224518.

XX PR 14-AUG-2000; 2000US-0224519.

XX PR 14-AUG-2000; 2000US-0225213.

XX PR 14-AUG-2000; 2000US-0225214.

XX PR 14-AUG-2000; 2000US-0225266.

XX PR 14-AUG-2000; 2000US-0225267.

XX PR 14-AUG-2000; 2000US-0225268.

XX PR 14-AUG-2000; 2000US-0225270.

XX PR 14-AUG-2000; 2000US-0225447.

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XX PR 14-AUG-2000; 2000US-0225758.

XX PR 18-AUG-2000; 2000US-0226279.

XX PR 22-AUG-2000; 2000US-0226681.

XX PR 22-AUG-2000; 2000US-0226688.

XX PR 22-AUG-2000; 2000US-0227182.

XX PR 23-AUG-2000; 2000US-0227009.

XX PR 30-AUG-2000; 2000US-0228924.

XX PR 01-SEP-2000; 2000US-0229287.

XX PR 01-SEP-2000; 2000US-0229343.

XX PR 01-SEP-2000; 2000US-0229345.

XX PR 05-SEP-2000; 2000US-0229509.

XX PR 06-SEP-2000; 2000US-0229513.

XX PR 06-SEP-2000; 2000US-0230437.

PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
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PR 08-SEP-2000; 2000US-0232080.
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PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
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PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
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PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
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PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
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PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
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PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
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PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
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PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
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PR 17-NOV-2000; 2000US-0249218.

PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 06-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

Disclosure; SEQ ID NO 39925; 3071bp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I) amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patient's own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/hematopoietic-related diseases, especially cancers and cancer metastases of hematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/hematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAK82169 represent sequences used in the exemplification of the present invention.

SQ Sequence 98 BP; 18 A; 27 C; 36 G; 17 T; 0 other;

Query Match 1.6%; Score 38; DB 22; Length 98;

Best Local Similarity 100.0%; Pred. No. 5.4e-08;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2334 GGCCTCCCAAGTCTGGGATTACAGGATGAGCCACC 2371

|||||

DB 50 GGCCTCCCAAGTCTGGGATTACAGGATGAGCCACC 13

Search completed: January 11, 2003, 07:12:37

Job time : 492 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 11, 2003, 06:06:17 ; Search time 88 Seconds

(without alignments)

8266.333 Million cell updates/sec

Title: US-10-005-344-1

Perfect score: 2372

Sequence: 1 gaccgcgcagcttgctg.....attacagcgatgacccagc 2372

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 687286

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA.*

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*

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5: /cgn2_6/ptodata/2/ina/PTCUS_COMB.seq.*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	73	3.1	73	3	US-09-073-567-49
2	39	1.6	85	2	US-08-454-557C-92
3	39	1.6	85	2	US-08-340-426D-92
4	39	1.6	85	2	US-08-450-673C-92
5	39	1.6	85	5	PCT-US95-17111A-92
6	35	1.5	40	4	US-09-540-699-17
7	30	1.3	40	4	US-09-060-023A-1
c 8	29	1.2	29	4	US-09-540-699-20
9	29	1.2	60	2	US-08-454-557C-57
10	29	1.2	60	2	US-08-340-426D-57
11	29	1.2	60	2	US-08-450-673C-57
12	29	1.2	60	5	PCT-US95-17111A-57
13	29	1.2	76	2	US-08-454-557C-69
14	29	1.2	76	2	US-08-340-426D-69
15	29	1.2	76	2	US-08-450-673C-69
16	29	1.2	76	5	PCT-US95-17111A-69
17	28	1.2	28	2	US-08-859-998-27
c 18	28	1.2	28	2	US-08-859-998-28
19	28	1.2	28	4	US-09-225-928-27
c 20	28	1.2	28	4	US-09-225-928-28
21	28	1.2	28	4	US-09-540-699-16
c 22	26	1.1	26	4	US-09-280-805-270
23	26	1.1	26	4	US-09-540-699-18
24	26	1.1	35	1	US-08-255-889-10
25	25	1.1	25	4	US-09-280-805-271
26	25	1.1	25	4	US-09-837-149-4
27	25	1.1	25	4	US-09-357-740-14

28	25	1.1	75	4	US-09-357-740-15	Sequence 15, Appl
29	24	1.0	30	4	US-09-480-718-28	Sequence 28, Appl
30	24	1.0	39	4	US-09-480-718-33	Sequence 33, Appl
31	24	1.0	84	2	US-08-454-557C-91	Sequence 91, Appl
32	24	1.0	84	2	US-08-340-426D-91	Sequence 91, Appl
33	24	1.0	84	2	US-08-450-673C-91	Sequence 91, Appl
34	24	1.0	84	5	PCT-US95-17111A-91	Sequence 91, Appl
c 35	23	1.0	23	4	US-09-385-917-4	Sequence 4, Appl
36	23	1.0	30	4	US-09-480-718-35	Sequence 35, Appl
c 37	23	1.0	36	4	US-09-480-718-34	Sequence 34, Appl
c 38	23	1.0	47	4	US-09-641-638-659	Sequence 659, Appl
39	22	0.9	22	1	US-08-635-820A-1	Sequence 1, Appl
40	22	0.9	22	3	US-09-100-104-1	Sequence 3, Appl
41	22	0.9	22	4	US-09-385-917-3	Sequence 19, Appl
c 42	22	0.9	22	4	US-09-540-699-19	Sequence 31, Appl
c 43	22	0.9	30	4	US-09-480-718-31	Sequence 28, Appl
c 44	21	0.9	21	1	US-08-753-147-28	Sequence 22, Appl
45	21	0.9	21	3	US-09-073-567-22	

ALIGNMENTS

RESULT 1
US-09-073-567-49/c
; Sequence 49, Application US/09073567
; Patent No. 6013786
; GENERAL INFORMATION:
; APPLICANT: Jiaodong Chen
; APPLICANT: Sudhir Agrawal
; APPLICANT: Ruiwen Zhang
; TITLE OF INVENTION: MDM2-SPECIFIC ANTISENSE OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: United States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 97
; CURRENT APPLICATION DATA: US/09/073,567
; APPLICATION NUMBER: US/09/073,567
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Greenfield, Michael S.
; REGISTRATION NUMBER: 37,147
; REFERENCE/DOCKET NUMBER: 98,057-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 913-0001
; TELEFAX: (312) 913-0002
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 73 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: nucleic acid
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
US-09-073-567-49

Query Match 3.1%; Score 73; DB 3; Length 73;
Best Local Similarity 100.0%; Pred. No. 6.7e-24;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 665 AGGTACATCTCTGAGTCAGACAGGTCACCTTGAGGTGGGAGTGATCAAAAGGACCT 724
|||||

US-08-450-673C-92

Query Match 1.6%; Score 39; DB 2; Length 85;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2290 GCCAGGATGCTCGATCTCTGACCTCGTGATCGGCC 2328
|||||
DB 9 GCCAGGATGCTCGATCTCTGACCTCGTGATCGGCC 47

RESULT 5

PCT-US95-17111A-92
; Sequence 92, Application PC/TUS9517111A
; GENERAL INFORMATION:
; APPLICANT: Wands, Jack R.
; APPLICANT: de la Monte, Suzanne
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and
; TITLE OF INVENTION: Detection of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA: PCT/US95/17111A

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/340,426

FILING DATE: 14-NOV-1994

ATTORNEY/AGENT INFORMATION:

NAME: Ludwig, Steven R.

REGISTRATION NUMBER: 36,203

REFERENCE/DOCKET NUMBER: 0609.3840002

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 92:

SEQUENCE CHARACTERISTICS:

LENGTH: 85 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: both

PCT-US95-17111A-92

Query Match 1.6%; Score 39; DB 5; Length 85;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2290 GCCAGGATGCTCGATCTCTGACCTCGTGATCGGCC 2328
|||||
DB 9 GCCAGGATGCTCGATCTCTGACCTCGTGATCGGCC 47

RESULT 6

US-09-540-699-17

; Sequence 17, Application US/09540699

; Patent No. 6383752

; GENERAL INFORMATION:

; APPLICANT: Agrawal, Sudhir

; APPLICANT: Kandimalia, Ekambar R.

; TITLE OF INVENTION: Pseudo-Cyclic Oligonucleobases

; FILE REFERENCE: 99,128-B

; CURRENT APPLICATION NUMBER: US/09/540,699

; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,138
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 60/174,642
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Oligonucleotide
; OTHER INFORMATION: that is complementary to a portion of the human
; OTHER INFORMATION: MDM2 mRNA
US-09-540-699-17

Query Match 1.3%; Score 35; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 664 CAGGTACATCTGTGAGTGAGACAGGTGTACCTT 698
|||||
DB 6 CAGGTACATCTGTGAGTGAGACAGGTGTACCTT 40

RESULT 7

US-09-060-023A-1/c
; Sequence 1, Application US/09060023A
; Patent No. 6391642
; GENERAL INFORMATION:
; APPLICANT: Resnick, Michael A.
; APPLICANT: Larionov, Vladimir L.
; APPLICANT: Kourina, Natalay Y.
; APPLICANT: Perkins, Edward L.
; TITLE OF INVENTION: TRANSFORMATION-ASSOCIATED RECOMBINATION
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Needle & Rosenberg, P.C.
; STREET: Suite 1200, 127 Peachtree Street, N.E.
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303-1811

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/060,023A

FILING DATE: April 14, 1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/11478

FILING DATE: July 9, 1996

ATTORNEY/AGENT INFORMATION:

NAME: Perryman, David G.

REGISTRATION NUMBER: 33,438

REFERENCE/DOCKET NUMBER: 14014.0291

TELECOMMUNICATION INFORMATION:

TELEPHONE: 404-688-0770

TELEFAX: 404-688-9880

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 40 bases

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-09-060-023A-1

Query Match 1.3%; Score 30; DB 4; Length 40;

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Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2332 TCGGCTCCCAAGTCTGGGATTACAGGC 2361
|||||
Db 40 TCGGCTCCCAAGTCTGGGATTACAGGC 11

RESULT 8
US-09-540-699-20/c
; Sequence 20, Application US/09540699
; Patent No. 6383752
; GENERAL INFORMATION:
; APPLICANT: Agrawal, Sudhir
; APPLICANT: Kandimala, Ekambar R.
; TITLE OF INVENTION: Pseudo-Cyclic Oligonucleobases
; FILE REFERENCE: 99,128-B
; CURRENT APPLICATION NUMBER: US/09/540,699
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,138
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 60/174,642
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: MDM2 mRNA
; OTHER INFORMATION: probe: +338 to +389.
US-09-540-699-20

Query Match 1.2%; Score 29; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.00084;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 649 AGGAATCATCGGACTCAGGTACATCTGTG 677
|||||
Db 29 AGGAATCATCGGACTCAGGTACATCTGTG 1

RESULT 9
US-08-454-557C-57
; Sequence 57, Application US/08454557C
; Patent No. 5830670
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; APPLICANT: Wands, Jack R.
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
; FILE REFERENCE: 0609.3840003
; CURRENT APPLICATION NUMBER: US/08/454,557C
; PRIOR FILING DATE: 30-MAY-1995
; PRIOR APPLICATION NUMBER: 514
; CLASSIFICATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840003

Query Match 1.2%; Score 29; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 0.00081;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2260 TTTTAGTAGACAGGTTTCACCGTGT 2288
|||||
Db 25 TTTTAGTAGACAGGTTTCACCGTGT 53

RESULT 10
US-08-340-426D-57
; Sequence 57, Application US/08340426D
; Patent No. 5948634
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; APPLICANT: Wands, Jack R.
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
; FILE REFERENCE: 0609.3840002
; CURRENT APPLICATION NUMBER: US/08/340,426D
; PRIOR FILING DATE: 14-NOV-1994
; PRIOR APPLICATION NUMBER: 435
; CLASSIFICATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840002

Query Match 1.2%; Score 29; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 0.00081;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2260 TTTTAGTAGACAGGTTTCACCGTGT 2288
|||||
Db 25 TTTTAGTAGACAGGTTTCACCGTGT 53

RESULT 11
US-08-450-673C-57
; Sequence 57, Application US/08450673C
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
US-08-454-557C-57

Query Match 1.2%; Score 29; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 0.00081;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2260 TTTTAGTAGACAGGTTTCACCGTGT 2288
|||||
Db 25 TTTTAGTAGACAGGTTTCACCGTGT 53

RESULT 10
US-08-340-426D-57
; Sequence 57, Application US/08340426D
; Patent No. 5948634
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; APPLICANT: Wands, Jack R.
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
; FILE REFERENCE: 0609.3840002
; CURRENT APPLICATION NUMBER: US/08/340,426D
; PRIOR FILING DATE: 14-NOV-1994
; PRIOR APPLICATION NUMBER: 435
; CLASSIFICATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840002

Query Match 1.2%; Score 29; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 0.00081;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2260 TTTTAGTAGACAGGTTTCACCGTGT 2288
|||||
Db 25 TTTTAGTAGACAGGTTTCACCGTGT 53

RESULT 11
US-08-450-673C-57
; Sequence 57, Application US/08450673C
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; Patent No. 5948888
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; NAME: Ludwig, Jack R.
; TITLE OF INVENTION: Neural Thread protein Gene Expression and Detection
; TITLE OF INVENTION: of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,673C
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609,3840004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; US-08-450-673C-57

Query Match 1.2%; Score 29; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 0.00081;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2260 TTTTAGTAGACAGCGGTTTCACCGTGT 2288
Db 25 TTTTAGTAGACAGCGGTTTCACCGTGT 53

RESULT 12
PCT-US95-17111A-57
; Sequence 57: Application PC/TUS9517111A
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; NAME: Ludwig, Jack R.
; TITLE OF INVENTION: Neural Thread protein Gene Expression and
; TITLE OF INVENTION: Detection of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/17111A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/340,426
; FILING DATE: 14-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609,3840002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; PCT-US95-17111A-57

Query Match 1.2%; Score 29; DB 5; Length 60;
Best Local Similarity 100.0%; Pred. No. 0.00081;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2260 TTTTAGTAGACAGCGGTTTCACCGTGT 2288
Db 25 TTTTAGTAGACAGCGGTTTCACCGTGT 53

RESULT 13
US-08-454-557C-69
; Sequence 69: Application US/08454557C
; Patent No. 5830670
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; NAME: Wands, Jack R.
; TITLE OF INVENTION: Neural Thread protein Gene Expression and Detection
; TITLE OF INVENTION: of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,557C
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609,3840003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 76 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; US-08-454-557C-69

Query Match 1.2%; Score 29; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 0.0008;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2260 TTTTAGTAGACAGCGGTTTCACCGTGT 2288
Db 25 TTTTAGTAGACAGCGGTTTCACCGTGT 53

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Db 25 TTTTAGTAGACAGGGTTTCACCGTGT 53

RESULT 14
US-08-340-426D-69
; Sequence 69, Application US/08340426D
; Patent No. 5948634
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; APPLICANT: Wands, Jack R.
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
; TITLE OF INVENTION: of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340,426D
; FILING DATE: 14-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 76 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
;
US-08-340-426D-69

Query Match 1.2%; Score 29; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 0.0008;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2260 TTTTAGTAGACAGGGTTTCACCGTGT 2288
|||||
Db 25 TTTTAGTAGACAGGGTTTCACCGTGT 53

Search completed: January 11, 2003, 08:57:11
Job time : 90 secs

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/450,673C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840004
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 76 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
US-08-450-673C-69

Query Match 1.2%; Score 29; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 0.0008;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2260 TTTTAGTAGACAGGGTTTCACCGTGT 2288
|||||
Db 25 TTTTAGTAGACAGGGTTTCACCGTGT 53

Search completed: January 11, 2003, 08:57:11
Job time : 90 secs

US-08-450-673C-69
; Sequence 69, Application US/08450673C
; Patent No. 5948688
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; APPLICANT: Wands, Jack R.
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
; TITLE OF INVENTION: of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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OM nucleic - nucleic search, using sw model

Run on: January 11, 2003, 06:08:32 ; Search time 108 Seconds
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Title: US-10-005-344-1

Perfect score: 2372

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Gapop 60.0 , Gapext 60.0

Searched: 389086 seqs, 220051671 residues

Word size : 0

Total number of hits satisfying chosen parameters: 239302

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database :

Published Applications_NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	43	1.8	92	10	US-09-761-288-37
C 2	42	1.8	87	10	US-09-764-877-3775
C 3	37	1.6	94	10	US-09-761-288-52
C 4	32	1.3	92	10	US-09-761-288-33
C 5	32	1.3	94	10	US-09-761-288-41
C 6	32	1.3	94	10	US-09-761-288-48
C 7	29	1.2	96	10	US-09-761-288-47
C 8	29	1.2	98	10	US-09-764-847-1866
C 9	29	1.2	98	10	US-09-764-847-1867
C 10	28	1.2	28	10	US-09-225-201-27
C 11	28	1.2	28	10	US-09-225-201-28
C 12	28	1.2	84	10	US-09-920-300A-1278
C 13	28	1.2	84	12	US-10-033-528-1278
C 14	28	1.2	88	10	US-09-764-869-1719
C 15	28	1.2	84	10	US-09-764-860-1052
C 16	27	1.1	84	10	US-09-764-860-1053
C 17	27	1.1	87	10	US-09-764-869-1866
C 18	27	1.1	87	10	US-09-764-860-766
C 19	27	1.1	87	10	US-09-764-860-962

C 20	27	1.1	87	10	US-09-764-877-2984
C 21	26	1.1	26	9	US-10-006-922-19
C 22	26	1.1	26	10	US-09-752-983-270
C 23	26	1.1	69	10	US-09-815-343-348
C 24	26	1.1	98	10	US-09-764-860-818
C 25	26	1.1	98	10	US-09-764-860-819
C 26	25	1.1	25	10	US-09-752-983-271
C 27	25	1.1	41	9	US-10-006-922-21
C 28	25	1.1	100	10	US-09-764-860-720
C 29	24	1.0	32	10	US-09-214-371-71
C 30	24	1.0	32	10	US-09-214-371-69
C 31	24	1.0	86	10	US-09-764-887-565
C 32	24	1.0	89	10	US-09-764-887-567
C 33	24	1.0	90	9	US-09-764-904-79
C 34	24	1.0	90	9	US-09-764-904-80
C 35	24	1.0	90	9	US-09-764-904-81
C 36	24	1.0	90	10	US-09-764-860-607
C 37	24	1.0	90	10	US-09-764-860-608
C 38	24	1.0	90	10	US-09-764-860-609
C 39	24	1.0	95	9	US-09-764-868-1444
C 40	24	1.0	96	10	US-09-764-887-554
C 41	24	1.0	100	10	US-09-764-887-560
C 42	24	1.0	100	10	US-09-908-711-136
C 43	24	1.0	100	10	US-09-764-869-1674
C 44	23	1.0	23	10	US-09-884-898-4
C 45	23	1.0	84	10	US-09-764-869-2102

ALIGNMENTS

RESULT 1

US-09-761-288-37/c
; Sequence 37, Application US/09761288
; Patent No. US20020065405A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Prayaga, Sudhirdas
; APPLICANT: Taupier, Raymond J
; APPLICANT: Mishra, Vishnu
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberky
; APPLICANT: Li, Li
; TITLE OF INVENTION: NO. US20020065405A1el Polypeptides and Nucleic Acids Encoding

FILE REFERENCE: 15966-638
; CURRENT APPLICATION NUMBER: US/09761,288
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/177,839
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/176,134
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/175,989
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: 60/218,324
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/220,253
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: 60/178,191
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: 60/178,227
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: 60/220,590
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 92
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-761-288-37

Query Match 1.8%; Score 43; DB 10; Length 92;
Best Local Similarity 100.0%; Pred. No. 5.1e-11;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2319 TGATCCGCCACCTCGGCTCCCAAGTCTGGGATTACAGGC 2361
|||||
Db 59 TGATCCGCCACCTCGGCTCCCAAGTCTGGGATTACAGGC 17

RESULT 2

US-09-764-877-3775/c
; Sequence 3775, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3775
; LENGTH: 87
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3775

Query Match 1.8%; Score 42; DB 10; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2319 TGATCCGCCACCTCGGCTCCCAAGTCTGGGATTACAGG 2360
|||||
Db 48 TGATCCGCCACCTCGGCTCCCAAGTCTGGGATTACAGG 7

RESULT 3

US-09-761-288-52
; Sequence 52, Application US/09761288
; Patent No. US20020065405A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Prayaga, Sudhirdas
; APPLICANT: Taupier, Raymond J
; APPLICANT: Mishra, Vishnu
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Li, Li
; TITLE OF INVENTION: No. US20020065405A1el Polypeptides and Nucleic Acids Encoding Sam
; FILE REFERENCE: 15966-638
; CURRENT APPLICATION NUMBER: US/09/761,288
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/177,839
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/176,134
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/175,989
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: 60/218,324
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/178,191
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: 60/220,253
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: 60/178,191
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: 60/220,590
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52
; LENGTH: 94
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-761-288-52

Query Match 1.6%; Score 37; DB 10; Length 94;
Best Local Similarity 100.0%; Pred. No. 4.2e-08;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2334 GGCCTCCCAAGTCTGGGATTACAGGATGAGCCAC 2370
|||||
Db 49 GGCCTCCCAAGTCTGGGATTACAGGATGAGCCAC 85

RESULT 4

US-09-761-288-33/c
; Sequence 33, Application US/09761288
; Patent No. US20020065405A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Prayaga, Sudhirdas
; APPLICANT: Taupier, Raymond J
; APPLICANT: Mishra, Vishnu
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Li, Li
; TITLE OF INVENTION: No. US20020065405A1el Polypeptides and Nucleic Acids Encoding
; FILE REFERENCE: 15966-638
; CURRENT APPLICATION NUMBER: US/09/761,288
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/177,839
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/176,134
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/175,989
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: 60/218,324
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/220,253
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: 60/178,191
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: 60/178,227
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: 60/220,590
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 92
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-761-288-33

Query Match 1.3%; Score 32; DB 10; Length 92;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2286 GTTAGCCAGGATGGTCTCGATCTCTGACCTC 2317
|||||
Db 92 GTTAGCCAGGATGGTCTCGATCTCTGACCTC 61

RESULT 5

US-09-761-288-41/c
; Sequence 41, Application US/09761288
; Patent No. US20020065405A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Prayaga, Sudhirdas
; APPLICANT: Taupier, Raymond J
; APPLICANT: Mishra, Vishnu
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Li, Li
; TITLE OF INVENTION: No. US20020065405A1el Polypeptides and Nucleic Acids Encoding

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; FILE REFERENCE: 15966-638
; CURRENT APPLICATION NUMBER: US/09/761,288
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/177,839
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/176,134
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/175,989
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: 60/218,324
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/220,253
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: 60/178,191
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: 60/178,227
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: 60/220,590
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 94
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-761-288-41
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Query Match 1.3%; Score 32; DB 10; Length 94;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 2286 GTTAGCCAGGATGCTCGATCTCTCGACCTC 2317
      |||||
DB 94 GTTAGCCAGGATGCTCGATCTCTCGACCTC 63
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RESULT 6

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US-09-761-288-48
; Sequence 48, Application US/09761288
; Patent No. US20020065405A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Prayaga, Sudhirdas
; APPLICANT: Taupier, Raymond J
; APPLICANT: Mishra, Vishnu
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Li, Li
; TITLE OF INVENTION: No. US20020065405A1el Polypeptides and Nucleic Acids Encoding Sam
```

```
; FILE REFERENCE: 15966-638
```

```
; CURRENT APPLICATION NUMBER: US/09/761,288
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/177,839
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/176,134
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/175,989
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: 60/218,324
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/220,253
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: 60/178,191
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: 60/178,227
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: 60/220,590
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 94
; TYPE: DNA
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; ORGANISM: Homo sapiens
US-09-761-288-48
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Query Match 1.3%; Score 32; DB 10; Length 94;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 2286 GTTAGCCAGGATGCTCGATCTCTCGACCTC 2317
      |||||
DB 1 GTTAGCCAGGATGCTCGATCTCTCGACCTC 32
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RESULT 7

```
US-09-761-288-47/c
; Sequence 47, Application US/09761288
; Patent No. US20020065405A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Prayaga, Sudhirdas
; APPLICANT: Taupier, Raymond J
; APPLICANT: Mishra, Vishnu
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Li, Li
; TITLE OF INVENTION: No. US20020065405A1el Polypeptides and Nucleic Acids Encoding
```

```
; FILE REFERENCE: 15966-638
; CURRENT APPLICATION NUMBER: US/09/761,288
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/177,839
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/176,134
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/175,989
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: 60/218,324
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/220,253
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: 60/178,191
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: 60/178,227
; PRIOR FILING DATE: 2000-01-26
; PRIOR APPLICATION NUMBER: 60/220,590
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 96
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-761-288-47
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Query Match 1.2%; Score 29; DB 10; Length 96;
Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 2330 CCTCGCCCTCCAAAGTCTGGATTACA 2358
      |||||
DB 50 CCTCGCCCTCCAAAGTCTGGATTACA 22
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RESULT 8

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US-09-764-847-1866/c
; Sequence 1866, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
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;
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
; SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-225-201-28

Query Match          1.2%; Score 28; DB 10; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1204 CCTAGCTGACTATTGGAATGCACATTC 1231
Db 28 CCTAGCTGACTATTGGAATGCACATTC 1

RESULT 12
US-09-920-300A-1278
; Sequence 1278, Application US/09920300A
; Patent No. US20020136728A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: SECRIST, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.547
; CURRENT APPLICATION NUMBER: US/09/920,300A
; CURRENT FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 1789
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1278
; LENGTH: 84
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-920-300A-1278

Query Match          1.2%; Score 28; DB 10; Length 84;
Best Local Similarity 100.0%; Pred. No. 0.00096;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2330 CCTCGGCTCCCAAGTCTGGGATTAC 2357
Db 40 CCTCGGCTCCCAAGTCTGGGATTAC 67

RESULT 13
US-10-033-528-1278
; Sequence 1278, Application US/10033528
; Patent No. US20020131971A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: SECRIST, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.547C1
; CURRENT APPLICATION NUMBER: US/10/033,528
; CURRENT FILING DATE: 2001-12-26
; NUMBER OF SEQ ID NOS: 1896
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1278
; LENGTH: 84
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-528-1278

Query Match          1.2%; Score 28; DB 12; Length 84;
Best Local Similarity 100.0%; Pred. No. 0.00096;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2330 CCTCGGCTCCCAAGTCTGGGATTAC 2357
Db 27 CCTCGGCTCCCAAGTCTGGGATTAC 1

Search completed: January 11, 2003, 08:59:12
Job time : 109 secs
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Db 40 CCTCGGCTCCCAAGTCTGGGATTAC 67

RESULT 14
US-09-764-869-1719
; Sequence 1719, Application US/09764869
; Patent No. US20020061521A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/764,869
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1719
; LENGTH: 88
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-869-1719

Query Match          1.2%; Score 28; DB 10; Length 88;
Best Local Similarity 100.0%; Pred. No. 0.00096;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2330 CCTCGGCTCCCAAGTCTGGGATTAC 2357
Db 61 CCTCGGCTCCCAAGTCTGGGATTAC 88

RESULT 15
US-09-764-860-1052/c
; Sequence 1052, Application US/09764860
; Patent No. US20020094953A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC008
; CURRENT APPLICATION NUMBER: US/09/764,860
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1198
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1052
; LENGTH: 84
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-860-1052

Query Match          1.1%; Score 27; DB 10; Length 84;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2330 CCTCGGCTCCCAAGTCTGGGATTAC 2356
Db 27 CCTCGGCTCCCAAGTCTGGGATTAC 1

Search completed: January 11, 2003, 08:59:12
Job time : 109 secs
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2000

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 11, 2003, 03:15:17 ; Search time 3329 Seconds

(without alignments)
11539.710 Million cell updates/sec

Title: US-10-005-344-1

Perfect score: 2372

Sequence: 1 gcaccgcgcagcttgctg.....attacagcatgagccacg 2372

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 15154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 357874

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database :

EST.*

- 1: em_estba.*
- 2: em_esthum.*
- 3: em_estin.*
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- 5: em_estov.*
- 6: em_estpl.*
- 7: em_estro.*
- 8: em_hic.*
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- 10: gb_est2.*
- 11: gb_hic.*
- 12: gb_est3.*
- 13: gb_est4.*
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- 17: gb_gss.*
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- 19: em_gss_inv.*
- 20: em_gss_pln.*
- 21: em_gss_vit.*
- 22: em_gss_fun.*
- 23: em_gss_mam.*
- 24: em_gss_mus.*
- 25: em_gss_other.*
- 26: em_gss_pro.*
- 27: em_gss_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	ID	Description
C 1	43	1.8	100	13	BC983527
C 2	41	1.7	50	9	AU104029
C 3	41	1.7	55	10	AW059824
C 4	38	1.6	93	10	AW275505
C 5	38	1.6	94	10	AW235474
C 6	37	1.6	37	14	R70733

C 7	1.6	80	14	F24490
C 8	1.6	90	17	A2756775
C 9	1.5	54	17	BH70627
C 10	1.5	61	17	A275874
C 11	1.5	74	9	AA078709
C 12	1.5	59	9	AA082835
C 13	1.5	84	10	BE515208
C 14	1.5	35	96	AA078527
C 15	1.4	34	9	AU102534
C 16	1.3	32	14	N84707
C 17	1.3	32	17	AQ092880
C 18	1.3	32	88	AA080831
C 19	1.3	32	96	R67088
C 20	1.3	31	50	AU103190
C 21	1.3	30	14	F34634
C 22	1.3	87	14	T87662
C 23	1.3	100	12	BG099457
C 24	1.2	29	97	BG152006
C 25	1.2	29	100	A2757131
C 26	1.2	28	87	AA078171
C 27	1.1	28	14	R84946
C 28	1.1	54	9	AA457759
C 29	1.1	62	12	BG527934
C 30	1.1	62	12	BG776837
C 31	1.1	62	12	BG777129
C 32	1.1	72	17	A2575912
C 33	1.1	73	9	AA192407
C 34	1.1	87	10	AA063866
C 35	1.1	27	9	AA578401
C 36	1.1	34	14	N77004
C 37	1.1	45	9	AA807296
C 38	1.1	50	9	AU105707
C 39	1.1	87	14	D20989
C 40	1.1	100	12	BF675438
C 41	1.1	25	14	H46868
C 42	1.1	40	14	T69198
C 43	1.1	42	9	AA868654
C 44	1.1	46	9	AA912807
C 45	1.1	78	9	AA047357

ALIGNMENTS

RESULT 1
BG983527/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

PM0-CN0155-090301-004-al2 CN0155 Homo sapiens CDNA, mRNA sequence.
EST. human.
GI:14386262

PM0-CN0155-090301-004-al2 CN0155 Homo sapiens CDNA, mRNA sequence.
EST. human.
GI:14386262

PM0-CN0155-090301-004-al2 CN0155 Homo sapiens CDNA, mRNA sequence.
EST. human.
GI:14386262

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EST. human.
GI:14386262

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EST. human.
GI:14386262

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EST. human.
GI:14386262

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GI:14386262

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EST. human.
GI:14386262

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EST. human.
GI:14386262

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EST. human.
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GI:14386262

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EST. human.
GI:14386262

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GI:14386262

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EST. human.
GI:14386262

PM0-CN0155-090301-004-al2 CN0155 Homo sapiens CDNA, mRNA sequence.
EST. human.
GI:14386262

F24490 HSPD10834 H
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A275874 evi0d06.x
AA078709 7T0E11 C
AA082835 zn21g12.s
BE515208 601235919
AA078527 7P05B09 C
AU102534 AU102534
N84707 J0579F Huma
AQ092880 B06937-77
AA080831 oa40f11.s
R67088 y13oh05.s1
AU103190 AU103190
F34634 HSPD29754 H
T87662 yd91b12.s1
BG099457 naq44d08.
BG152006 naq72f02.
A2757131 ex05B01.r
AA078171 7H15B07 C
R84946 y165g08.r1
AA457759 aa92c06.r
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BG777129 602664345
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AA063866 DR0792.RR
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N77004 yv50f05.r1
AA807296 oc37c08.s
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D20989 HUMGS01971
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AA912807 ol43a05.s
AA047357 zl65h10.r

PM0-CN0155-090301-004-al2 CN0155 Homo sapiens CDNA, mRNA sequence.
EST. human.
GI:14386262

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GI:14386262

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GI:14386262

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GI:14386262

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GI:14386262

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GI:14386262

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GI:14386262

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EST. human.
GI:14386262

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EST. human.
GI:14386262

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EST. human.
GI:14386262

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EST. human.
GI:14386262

PM0-CN0155-090301-004-al2 CN0155 Homo sapiens CDNA, mRNA sequence.
EST. human.
GI:14386262

PM0-CN0155-090301-004-al2 CN0155 Homo sapiens CDNA, mRNA sequence.
EST. human.
GI:14386262

Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=PM04t2-PM0-CN0155-090301-004-a12t3-2001-03-09&t4=1)
 Seq primer: puc 18 forward
 High quality sequence stop: 99.

FEATURES

source
 Location/Qualifiers
 1..100
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="CN0155"
 /dev_stage="Adult"
 /note="Organ: colon normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
 34 a 24 c 22 g 19 t 1 others
 BASE COUNT
 ORIGIN
 Query Match 1.8%; Score 43; DB 13; Length 100;
 Best Local Similarity 100.0%; Pred. No. 6e-08;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2285 TGTAGCCAGGATGCTCGACGTCCTGACGTCGTCGATCGGCC 2327
 Db 45 TGTAGCCAGGATGCTCGACGTCCTGACGTCGTCGATCGGCC 3

RESULT 2
 AUI04029
 LOCUS AUI04029 Sugano Homo sapiens cDNA library EST 30-AUG-2001
 DEFINITION KAIR1572, mRNA sequence.
 ACCESSION AUI04029.1 GI:13553550
 VERSION AUI04029.1
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 50)
 AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
 TITLE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
 JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
 MEDLINE 21270072
 COMMENT Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp
 Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano ,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES

source
 Location/Qualifiers
 1..50
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="KAIR1572"
 /note="Differential display comparison of untreated and dimethylformate treated U937 cells"
 9 a 11 c 16 g 14 t
 BASE COUNT
 ORIGIN
 Query Match 1.7%; Score 41; DB 9; Length 50;
 Best Local Similarity 100.0%; Pred. No. 5.6e-07;

Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2274 GGTTTCACCGTGTAGCCAGGATGCTCGATCTCCCTGAC 2314
 Db 10 GGGTTTCACCGTGTAGCCAGGATGCTCGATCTCCCTGAC 50

RESULT 3

AW059824
 LOCUS AW059824 55 bp mRNA linear EST 23-AUG-2000
 DEFINITION LEBell.yg DNC15 Homo sapiens cDNA, mRNA sequence.
 ACCESSION AW059824
 VERSION AW059824.1 GI:6652146
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 55)
 AUTHORS Brenner,S., Williams,S.R., Vermass,E.H., Storck,T., Moon,K., McCollum,C., Mao,J.I., Kirchner,J.J., Eletr,S., DuBridge,R.B., Burcham,T. and Albrecht,G.
 TITLE In vitro cloning of complex mixtures of DNA on microbeads: Physical separation of differentially expressed cDNAs
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)
 MEDLINE 20144098
 COMMENT Contact: Burcham TS
 LYNX Therapeutics, Inc.
 25861 Industrial Blvd., Hayward, CA 94545, USA
 Tel: 510 670 9338
 Fax: 510 670 9302
 Email: timbelynxgen.com
 Sequence obtained from LYNX Therapeutics Megasort technology. Collected from the down-regulated gate.
 High quality sequence stop: 55.

FEATURES

source
 Location/Qualifiers
 1..55
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="DNC15"
 /cell_type="monocytic leukemia"
 /note="Vector: PCR2.1; Cloning of PCR products from micro-beads carrying 3' end of down-regulated cDNA. THP-1 cells non-induced (treated with DMSO only)."
 11 a 19 c 15 g 10 t
 BASE COUNT
 ORIGIN
 Query Match 1.7%; Score 41; DB 10; Length 55;
 Best Local Similarity 100.0%; Pred. No. 5.5e-07;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2320 GATCCGCCACCTCGGCTCCCAAGTCCTGGATTACAGG 2360
 Db 1 GATCCGCCACCTCGGCTCCCAAGTCCTGGATTACAGG 41

RESULT 4

AW275505/c
 LOCUS AW275505 93 bp mRNA linear EST 03-JAN-2000
 DEFINITION xh08f10.x1 NCI_CGAP_Li5 Homo sapiens cDNA clone IMAGE:2693131 3', similar to contains Alu repetitive element., mRNA sequence.
 ACCESSION AW275505
 VERSION AW275505.1 GI:6662458
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 93)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

```
Location/Qualifiers .
  i. 94
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone_image="2693419"
    /clone_lib="NCI_CGAP_Li5"
    /tissue_type="hepatic adenoma"
    /lab_host="PH10a"
```

BASE COUNT
ORIGIN

Query Match 1.6%; Score 37; DB 14; Length 37;
 Best Local Similarity 100.0%; Pred. No. 3.7e-05;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2330 CCTCGCCCTCCCAAGTCTGGGATTACAGGCATGAG 2366
 Db 1 CCTCGCCCTCCCAAGTCTGGGATTACAGGCATGAG 37

RESULT 7
 F24490/c
 LOCUS HSPD10834 HM3 Homo sapiens cDNA clone s4000013A06, mRNA sequence.
 DEFINITION F24490
 ACCESSION F24490
 VERSION F24490.1 GI:4810116
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 80)
 AUTHORS Lanfranchi, G., Muraro, T., Caldara, F., Pacchioni, B., Pallavicini, A., Pandolfo, D., Toppo, S., Trevisan, S., Scarso, S. and Valie, G.
 TITLE Identification of 4370 expressed sequence tags from a 3'-end-specific cDNA library of human skeletal muscle by DNA sequencing and filter hybridization
 JOURNAL Genome Res. 6 (1), 35-42 (1996)
 MEDLINE 96276048
 COMMENT Contact: Valle G.
 CRIBI Biotechnology Centre
 University of Padua
 Via Trieste 75, 35121 Padua, Italy
 ABI Chromatograms and other information are available on WWW at
 http://group.bio.unipd.it.

FEATURES
 source
 1..80
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="s4000013A06"
 /clone_lib="HM3"
 /sex="female"
 /tissue_type="pectoral muscle (after mastectomy)"
 /note="Vector: pcDNAII (Invitrogen); Site 1: BstXI; Site 2: NotI. The library was constructed by G. Lanfranchi. This library is not subtracted nor normalized. The first strand cDNA was primed with a biotinylated oligo-dT-NotI primer (5'-biotin-AACCGGCTCGAGCGCCGCTTTTTTTTTTTT-3'). The ds cDNA was sonicated and size-selected in the range 350-550 bp. The 3' specific fragments were selected by streptavidin coated magnetic beads, ligated to non-palindromic BstXI adapters, NotI digested and directionally cloned into BstXI-NotI cut pcDNAII vector."

BASE COUNT 18 a 21 c 19 g 22 t
 ORIGIN

Query Match 1.6%; Score 37; DB 14; Length 80;
 Best Local Similarity 100.0%; Pred. No. 3e-05;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2334 GGCTCCCAAGTCTGGGATTACAGGCATGAGCCAC 2370
 Db 80 GGCTCCCAAGTCTGGGATTACAGGCATGAGCCAC 44

RESULT 8
 AZ756775
 LOCUS ew01e07.x1 PAX3/FKHR CASTING Library 'ew' Homo sapiens genomic
 DEFINITION AZ756775
 ACCESSION AZ756775
 VERSION AZ756775.1 GI:13176230
 KEYWORDS GSS.

SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 90)
 AUTHORS Barber, T.D., Barber, M.C., Tomescu, O., Barr, F.G., Ruben, S. and Friedman, T.B.
 TITLE Identification of Target Genes Regulated by PAX3 and PAX3--FKHR in Embryogenesis and Alveolar Rhabdomyosarcoma
 JOURNAL Genomics 79 (3), 278-284 (2002)
 MEDLINE 21853298
 COMMENT Contact: Friedman TB
 Laboratory of Molecular Genetics
 National Institute on Deafness and Other Communication Disorders,
 National Institute of Health
 5 Research Court, Room 2A-15, Rockville, MD 20850, USA
 Tel: 301 402 7580
 Fax: 301 496 7882
 Email: friedman@nidcd.nih.gov
 Plate: 01 row: e column: 07
 Seq primer: -21M13 forward primer (ABI)
 Class: Random plasmid subclone.
 Location/Qualifiers
 1..90
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="ew01e07"
 /clone_lib="PAX3/FKHR CASTING Library 'ew'"
 /sex="Male"
 /lab_host="DH10B"
 /note="Vector: pGEM-T Easy; Human genomic DNA was partially digested with Sau3AI, ligated to ds linkers, and enriched for binding to human PAX3/FKHR protein using a whole genome PCR-based strategy. DNA fragments containing putative PAX3/FKHR binding sites were amplified by PCR and cloned into pGEM-T Easy (Promega). The ligation products were transformed into DH10B electrocompetent cells (Life technologies)."

BASE COUNT 22 a 24 c 24 g 20 t
 ORIGIN

Query Match 1.6%; Score 37; DB 17; Length 90;
 Best Local Similarity 100.0%; Pred. No. 2.9e-05;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2325 GCCACCTCGGCTCCCAAGTCTGGGATTACAGGC 2361
 Db 10 GCCACCTCGGCTCCCAAGTCTGGGATTACAGGC 46

RESULT 9
 BH770627/c
 LOCUS LMGtag385 MG1363 Random Sequence Tag Library Lactococcus lactis
 DEFINITION BH770627
 ACCESSION BH770627.1 GI:20373584
 VERSION BH770627
 KEYWORDS GSS.
 SOURCE Lactococcus lactis subsp. cremoris.
 ORGANISM Lactococcus lactis subsp. cremoris
 Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 Lactococcus.
 REFERENCE 1 (bases 1 to 54)
 AUTHORS Bolotin, A., Ehrlich, S.D. and Sorokin, A.
 TITLE Studies of genomes of dairy bacteria Lactococcus lactis
 JOURNAL Sci. Aliments, (2002) In press
 COMMENT Contact: Sorokin A
 Genetique Microbienne
 INRA
 CRJ INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France
 Tel: 33 1 34 65 25 16
 Fax: 33 1 34 65 25 21
 Email: sorokine@jouy.inra.fr

best homologue in strain IL1403 is ynbD (46%)

Class: shotgun

High quality sequence start: 30

High quality sequence stop: 54.

FEATURES

source

Location/Qualifiers
1. .54
/organism="Lactococcus lactis subsp. cremoris"
/strain="MG1363"
/db_xref="taxon:1359"
/clone_lib="MG1363 Random Sequence Tag Library"
/note="Vector: pSGM2; Site_1: SmaI; Library of chromosomal fragments of L.lactis strain MG1363 was prepared by partial AluI digestion or by sonication."
8 a 16 c 21 g 9 t

BASE COUNT 8 a 16 c 21 g 9 t

ORIGIN

Query Match 1.5%; Score 36; DB 17; Length 54;
Best Local Similarity 100.0%; Pred. No. 9.3e-05;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2337 CTCCTCCAAAGTCTGGGATTACAGCATGAGCCACCG 2372

Db 43 CTCCTCCAAAGTCTGGGATTACAGCATGAGCCACCG 8

RESULT 10

AZ755874

LOCUS

DEFINITION ev10d06.x1 PAX3 CASTing Library 'ev' Homo sapiens genomic clone

ACCESSION AZ755874

VERSION AZ755874.1 GI:13175300

KEYWORDS GSS.

SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 61)

AUTHORS Barber,T.D., Barber,M.C., Tomescu,O., Barr,F.G., Ruben,S. and Friedman,T.B.

TITLE Identification of Target Genes Regulated by PAX3 and PAX3--FKHR in

Embryogenesis and Alveolar Rhabdomyosarcoma

Genomics 79 (3), 278-284 (2002)

JOURNAL 21853298

MEDLINE

COMMENT Laboratory of Molecular Genetics
National Institute on Deafness and Other Communication Disorders,
National Institutes of Health
5 Research Court, Room 2A-15, Rockville, MD 20850, USA
Tel: 301 402 7580
Fax: 301 496 7882
Email: friedman@nidcd.nih.gov
Plate: 10 row: d column: 06
Seg primer: -21M13 forward primer (ABI)
Class: random plasmid subclone.

FEATURES

source

Location/Qualifiers
1. .61
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ev10d06"
/clone_lib="PAX3 CASTing Library 'ev'"
/sex="Male"
/lab_host="DH10B"
/note="Vector: pGEM-T Easy; Human genomic DNA was partially digested with Sau3AI, ligated to ds linkers, and enriched for binding to human PAX3dQ+ protein using a whole genome PCR-based strategy. DNA fragments containing putative PAX3dQ+ binding sites were amplified by PCR and cloned into pGEM-T Easy (Promega). The ligation products were transformed into DH10B electrocompetent cells (Life Technologies)."
11 a 22 c 16 g 12 t

BASE COUNT

ORIGIN

Query Match 1.5%; Score 36; DB 17; Length 61;

Best Local Similarity 100.0%; Pred. No. 9e-05;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2326 CCCACCTCGGCTCCCAAAGTCTGGGATTACAGGC 2361

Db 18 CCCACCTCGGCTCCCAAAGTCTGGGATTACAGGC 53

RESULT 11

AA078709/c

LOCUS

DEFINITION 7T01E11 Chromosome 7 Thymus cDNA Library Homo sapiens cDNA clone

ACCESSION AA078709

VERSION AA078709.1 GI:1838204

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens

REFERENCE 1 (bases 1 to 74)

AUTHORS Touchman,J.W., Bouffard,G.G., Weintraub,L.A., Idol,J.R., Wang,L.,

Robbins,C.M., Nussbaum,J.C., Lovett,M. and Green,E.D.

TITLE 2006 expressed-sequence tags derived from human chromosome

JOURNAL Genome Res. 7 (3), 281-292 (1997)

MEDLINE 97228905

COMMENT Contact: Eric D. Green
Genome Technology Branch
National Human Genome Research Institute/NIH
49 Convent Dr., MSC4431, Building 49, Room 2A08, Bethesda, MD 20892
Tel: 3014020201
Fax: 3014024735
Email: egreen@nhgri.nih.gov
Plate: 01 row: E column: 11
Seg primer: -21M13 (ABI).

FEATURES

source

Location/Qualifiers
1. .74
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="7T01E11"
/clone_lib="Chromosome 7 Thymus cDNA Library"
/sex="mixture of female and male"
/tissue_type="thymus"
/dev_stage="1 week old (male), 11 year old (female)"
/lab_host="E. coli strain DH5 alpha"
/note="Organ: thymus; Vector: pAMP10; cDNA was generated from cytoplasmic RNA using a mixture of random DNA hexamers and oligo(dT). From this pool of cDNA, human chromosome 7-enriched cDNA was isolated by direct cDNA selection using chromosome 7 genomic DNA (cosmids). The resulting direct-selected cDNA was cloned into a plasmid vector using a non-directional uracil DNA glycosylase (UDG)-mediated cloning strategy."
19 a 17 c 22 g 16 t

BASE COUNT

ORIGIN

Query Match 1.5%; Score 36; DB 9; Length 74;

Best Local Similarity 100.0%; Pred. No. 8.5e-05;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2335 GCCTCCCAAGTCTGGGATTACAGGCATGAGCCAC 2370

Db 74 GCCTCCCAAGTCTGGGATTACAGGCATGAGCCAC 39

RESULT 12

AA082835

LOCUS

DEFINITION zn21g12.s1 Stragene neuroepithelium NT2RAMI 937234 Homo sapiens

CDNA clone IMAGE:548134 3' similar to contains Alu repetitive

BASE COUNT 59 bp mRNA linear EST 21-OCT-1996

element; mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

AA082835
AA082835.1 GI:1624910
EST.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS

1 (bases 1 to 59)
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissole,S., Dietrich,N., Dubuque,T., Favello,A., Gish,W., Hawkins
M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore
B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevaskis,E.,
Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)

TITLE
MEDLINE
COMMENT

97044478
Contact: Wilton RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40M13 fwd. from AmerSham.

FEATURES
source

1..59
Location/Qualifiers

/organism="Homo sapiens"
/db_xref="GDB:3926650"
/db_xref="taxon:9606"
/clone_lib="IMAGE:548134"
/clone_host="Ntera-2/RA-MI neuroepithelial cells"
/dev_stage="Ntera-2/RA-MI neuroepithelial cells"
/lab_host="SOLR (kanamycin resistant)"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Cloned unidirectionally. Primer: Oligo dT. NT2
(Ntera-2/cl.D1) precursor cells induced with Retinoic
Acid for 1 week, followed by 3 weeks in mitotic inhibitors
(Replate #2). Average insert size: 1.1 kb; Uni-ZAP XR
Vector; -5' adaptor sequence: 5' GAATTCGGCAGCAG 3' -3'
adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3"

BASE COUNT
ORIGIN

11 a 14 c 16 g 18 t

Query Match

Best Local Similarity 1.5%; Score 35; DB 9; Length 59;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2285

TGTTAGCAGGATGTCGATCTCTGACCTCGT 2319

Db 25

TGTTAGCAGGATGTCGATCTCTGACCTCGT 59

RESULT 13
BE515208/c

LOCUS
DEFINITION
601235919f1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608045 5',
mRNA sequence.

ACCESSION

BE515208

VERSION
KEYWORDS
SOURCE

BE515208.1 GI:9722423
EST.
human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS

1 (bases 1 to 84)
NIH-MGC http://mhc.nci.nih.gov/.

TITLE
JOURNAL

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM260 row: e column: 06

High quality sequence stop: 84.

FEATURES
source

Location/Qualifiers

1..84
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3608045"
/clone_lib="NIH_MGC_44"
/tissue_type="endometrium, adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pORF7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAGGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT
ORIGIN

21 a 21 c 29 g 13 t

Query Match

Best Local Similarity 1.5%; Score 35; DB 10; Length 84;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2290

GCACGATGTCGATCTCTGACCTCGTGATCC 2324

Db 59

GCACGATGTCGATCTCTGACCTCGTGATCC 25

RESULT 14
AA078527

LOCUS

7P05B09 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone

DEFINITION

7P05B09, mRNA sequence.

ACCESSION

AA078527

VERSION

AA078527.1 GI:1838015

KEYWORDS
SOURCE

EST.
human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

1 (bases 1 to 96)
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS

Touchman,J.W., Bouffard,G.G., Weintraub,L.A., Idol,J.R., Wang,L.,
Robbins,C.M., Nussbaum,J.C., Lovett,M. and Green,E.D.

TITLE

2006 expressed-sequence tags derived from human chromosome

JOURNAL

Genome Res. 7 (3), 281-292 (1997)

MEDLINE

97228905

COMMENT

Contact: Eric D. Green
Genome Technology Branch
National Human Genome Research Institute/NIH
49 Convent Dr., MSC4431, Building 49, Room 2A08, Bethesda, MD 20892
Tel: 3014020201
Fax: 3014024735
Email: egreen@nhgri.nih.gov
Plate: 05 row: B column: 09
Seq primer: -21M13 (AB1).

FEATURES
source

Location/Qualifiers

1..96
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="7P05B09"
/clone_lib="Chromosome 7 Placental cDNA Library"
/sex="female"
/dev_stage="placenta obtained at birth (full term)"
/lab_host="E. coli strain DH5 alpha"

/note="Organ: placenta; Vector: pAMP10; cDNA was generated from cytoplasmic RNA using a mixture of random DNA hexamers and oligo(dT). From this pool of cDNA, human chromosome 7-enriched cDNA was isolated by direct cDNA selection using chromosome 7 genomic DNA (cosmids). The resulting direct-selected cDNA was cloned into a plasmid vector using a non-directional uracil DNA glycosylase (UDG)-mediated cloning strategy."

BASE COUNT 25 a 29 c 20 g 22 t

ORIGIN

Query Match 1.5%; Score 35; DB 9; Length 96;

Best Local Similarity 100.0%; Pred. No. 0.00022;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2337 CTCCCAAGTCTGGGATTACAGGCATGAGCCACC 2371

|||||

Db 12 CTCCCAAGTCTGGGATTACAGGCATGAGCCACC 46

RESULT 15

AU102534

LOCUS

DEFINITION AU102534 Sugano Homo sapiens cDNA library EST 30-AUG-2001
ADSH00605, mRNA sequence.

ACCESSION AU102534

VERSION AU102534.1 GI:13552055

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 50)

AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata
, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki
, Y., Nakamura, Y., Suyama, A. and Sugano, S.

TITLE Diverse transcriptional initiation revealed by fine, large-scale

JOURNAL mapping of mRNA start sites

MEDLINE EMBO Rep. 2 (5), 388-393 (2001)

COMMENT 21270072

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
, S. Construction and characterization of a full length-enriched and

a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES Location/Qualifiers

1..50

source

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="ADSH00605"

/clone_lib="Sugano Homo sapiens cDNA library"

/note="Differential display comparison of untreated and

dimethylfumarate treated U937 cells"

BASE COUNT 10 a 18 c 13 g 9 t

ORIGIN

Query Match 1.4%; Score 34; DB 9; Length 50;

Best Local Similarity 100.0%; Pred. No. 0.00074;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2330 CTCGCGCTCCCAAGTCTGGGATTACAGGCAT 2363

|||||

Db 10 CTCGCGCTCCCAAGTCTGGGATTACAGGCAT 43

Search completed: January 11, 2003, 07:04:15

Job time : 3334 secs

